

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 ggctcgggcg gtgggtgggtc ggggtggcgcg ggtatcgctac aggtgcagct gaagcagctca 480  
 ggacctggcc tagtgcagtc ctacacagagc ctgtccatca cctgcacagt cctctggtttc 540  
 tcattaaacta ctattgctgt acactgggtt cgccagctctc caggaaaaggc tctggagtgg 600  
 ctgggagtgga tatggagtgg tggaaatcaca gactataatg cagctttcat atccagactg 660  
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720  
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactacc cttattactat 780  
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 <211> 1536  
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<220>  
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 tattttgattt ggtatctgca gaagccaggc cagctctctc agctcctgat ttatcagatg 240  
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 acactgagaa ctgcagaggt ggaagctgag gatgtgggtg ttattactg tgctcaaaat 360  
 ctgaaacttc cgctcacgtt cgggtctggg accaagctgg aggtgaaacg ggggtggcgt 420  
 ggctcgggcg gtgtgtggct ctacacagagc ctgtccatca cctgcacagt gaagcagctca 480  
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 tcattaaacta cctatctgtg acactgggtt gactataatg cagctttcat atccagactg 600  
 ctgggagtgga tatggagtgg tggaaatcaca gactataatg cagctttcat atccagactg 660  
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720  
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactacc cttattactat 780  
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<220>  
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 tccaaccttg cctcaggagt cccagacagg ttcatgagca gtgggtcagg aactgatttc 300  
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 ctgaaacttc cgctcacgtt cgggtctggg accaagctgg aggtgaaacg ggggtggcgt 420  
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 ggacctggcc tagtgcagtc acactgggtt gactataatg cagctttcat atccagactg 600  
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 aatgacacag ccatttatta actgggtgca aagccacagc agccacagc agccagcagc gggggagctg 900  
 gctatggact actgggtgca aaactcacac aagccacagc agccacagc agccagcagc gggggagctg 960  
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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acgtaccgtg tggtcagcgt cctcacgct ctgaccagg actggctgaa tggcaaggag 1140  
tacaagtcca aggtctccaa caaagccct ccagcccca tcgagaaaac catctccaaa 1200  
gccaaagggc agccccgaga accacaggtg tacaccctgc cccatccgc ggtatgagctg 1260  
accaagaacc aggtcagcct gacctgcctg gtcaaaagct tctatccag cgacatcgcc 1320  
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgc tccgtgctg 1380  
gactccgacg cctccttctt cctctacagc aagctcacg tggacaagag cagggtggcag 1440  
cagggggaacg gctctctatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500  
aagagccctt cctctgctcc gggtaaaagc gatccttcga acctgctccc atcctgggccc 1560  
attaccttaa tctcagtaaa tgggaatttt gtgatatgct gcctgacctt ctgctttgcc 1620  
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taaatcgata ctcgag 1696

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<211> 141  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 359  
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Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu  
35 40 45  
Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu  
50 55 60  
Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala  
65 70 75  
Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Ser Lys Ser Gln  
80 85 90  
Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr  
100 105 110  
Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met  
115 120 125  
Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
130 135 140

<210> 360  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 360  
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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr  
20 25 30  
Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu  
35 40 45  
Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Ile  
50 55 60  
Ser Arg Leu Ser Ile Thr Lys Asp Ser Lys Ser Gln Val Phe Phe  
65 70 75  
Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr Tyr Cys Ala  
80 85 90  
Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met Asp Tyr Trp  
100 105 110  
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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<210> 361  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 361  
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1 5 10 15  
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
20 25 30  
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser  
35 40 45  
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
50 55 60  
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
65 70 75  
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
85 90 95  
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
100 105 110  
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
115 120 125  
Leu Glu Leu Lys Arg  
130

<210> 362  
<211> 271  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 362  
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1 5 10 15  
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
20 25 30  
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser  
35 40 45  
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
50 55 60  
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
65 70 75  
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
85 90 95  
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
100 105 110  
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
115 120 125  
Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
130 135 140  
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
145 150 155 160  
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
165 170 175  
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys  
180 185 190  
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr  
195 200 205

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys  
 210 215 220  
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala  
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 260 265 270

<210> 363  
 <211> 505  
 <212> PRT  
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 <220>  
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<400> 363  
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 1 5 10 15  
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
 20 25 30  
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser  
 35 40 45  
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
 50 55 60  
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
 65 70 75 80  
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
 85 90 95  
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
 100 105 110  
 Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
 115 120 125  
 Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 130 135 140  
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
 145 150 155 160  
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
 165 170 175  
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys  
 180 185 190  
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr  
 195 200 205  
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys  
 210 215 220  
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala  
 225 230 235 240  
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr  
 245 250 255  
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
 260 265 270  
 Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Ser Pro  
 275 280 285  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 290 295 300  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 305 310 315 320  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 325 330 335  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 340 345 350  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 355 360 365  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 370 375 380  
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
385 390 395 400  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
405 410 415  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 430  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
485 490 495  
Lys Ser Leu Ser Leu Ser Pro Gly Lys  
500 505

<210> 364  
<211> 556  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 364  
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro  
20 25 30  
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser  
35 40 45  
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys  
50 55 60  
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala  
65 70 75  
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe  
85 90 95  
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
100 105 110  
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys  
115 120 125  
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly  
130 135 140  
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu  
145 150 155  
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe  
160 165 170  
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys  
175 180 185  
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr  
190 195 200  
Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Ser Lys  
205 210 215  
Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala  
220 225 230  
Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr  
235 240 245  
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
250 255 260  
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro  
265 270 275  
Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys  
280 285 290  
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
295 300 305  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Thr Tyr  
310 315 320  
325 330 335

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
340 345 350  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
355 360 365  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
370 375 380  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
385 390 400  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Ser Ser Arg Asp Glu Leu  
405 410 415  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 425 430  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
485 490 495  
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu  
500 505 510  
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile  
515 520 525  
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<210> 365

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to Y

<400> 365

gttggtgaag acgttccct gctgccacct gctctgtgcc acggtgagct tgctgtagag 60  
gtagaaggag cc 72

<210> 366

<211> 72

<212> DNA

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<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to A

<400> 366

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ggcgaaggag cc 72

<210> 367

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position  
407 XX to A

<400> 367

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gttggtgaag acgttcccct gctgccacct gctcttgcc acggtgagct tgctggcgag 60  
gaagaaggag cc 72

<210> 368  
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<223> 3' oligo to introduce mutation in CH3 at position  
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<400> 368  
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gtagaaggag cc 72

<210> 369  
<211> 72  
<212> DNA  
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<220>  
<223> 3' oligo to introduce mutation in CH3 at position  
405 XX to A and 407 to Y

<400> 369  
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ggcgaaggag cc 72

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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcttccgt gctggactcc 180  
gacggctcct tctacctcta tagcaagctc accgtggaca agagcagggt gcagcagggg 240  
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<210> 371  
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<220>  
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcttccgt gctggactcc 180  
gacggctcct tcgcccctcta tagcaagctc accgtggaca agagcagggt gcagcagggg 240  
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ctctccctgt ccccggttaa atga 324

<210> 372  
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<223> fusion polynucleotide

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tgggagagca	atgggacagc	ggagaaacaac	tacaagacca	cgctcccggt	gctggactcc	180
gacggtctct	ctctctcgc	cagcaagctc	accgtggaca	agagcagggt	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 373

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 373

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gacggtctct	ctctctcgc	cagcaagctc	accgtggaca	agagcagggt	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 374

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 374

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tgggagagca	atgggacagc	ggagaaacaac	tacaagacca	cgctcccggt	gctggactcc	180
gacggtctct	ctctctcgc	cagcaagctc	accgtggaca	agagcagggt	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
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<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 375

Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu
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Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
			20					25					30		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
			35				40					45			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
			50			55				60					
Tyr	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
65						70			75						
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
			85					90					95		



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100 105

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<211> 107  
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<220>  
<223> fusion polypeptide

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Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
20 25 30  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
35 40 45  
Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe  
50 55 60  
Ala Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
65 70 75 80  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
85 90 95  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 377  
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Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
20 25 30  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
35 40 45  
Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe  
50 55 60  
Phe Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
65 70 75 80  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
85 90 95  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 378  
<211> 107  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> fusion polypeptide

<400> 378  
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Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

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 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
 35 40 45  
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
 50 55 60  
 Tyr Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
 65 70 75 80  
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
 85 90 95  
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 100 105

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<220>  
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<400> 379  
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 20 25 30  
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
 35 40 45  
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
 50 55 60  
 Ala Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
 65 70 75 80  
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
 85 90 95  
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 100 105

<210> 380  
 <211> 1515  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

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 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcaactgg 180  
 taccagcaga agccaggatc ctcccccaaa cctctggatt atgcccattc caacctcgtt 240  
 tctggagctc ctgcttcgct cagttggcagt gggtctggga cctcttactc tctcaacaatc 300  
 agcagagtggt aggtctgaaga tgctgccaact tattactgcc agcagtgtag ctttaaccaca 360  
 cccaagtttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc ggcgcgggtg 420  
 gggatctggag gaggttgggag ctctcaggct tatctacagc agtctggggc tggagtggtg 480  
 aggcctgggg ctgctagtgaa gatgtcctgc aaggctcttg gctacacatt taccagttac 540  
 aatatgcact gggtaaaagca gacacctaga cagggtcctg aatggattgg agctatttat 600  
 ccaggaaattg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaaaatctt ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctcgg 720  
 gtctattttct gtcacaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 ggacacaggga ccacgtctcc cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840  
 cacacatccc caaggacac agcacctgaa ctctctgggg gaccgtcagt ctctctcttc 900  
 ccccaaaaac cctcatgatc tcccgagacc ctgaggtcac atgcgtgggt 960  
 gtggagctga gccacgaaga ccttgaggac aagttcaact ggtacgtgga cggcgtggag 1020  
 gtgcataatg ccaagacaaa ccgcggggag gaggagtaca acagcacgta cgtgtgggtc 1080  
 agcgtcctca cgtctctgca ccaggactgg ctgaaatggca agggagtacaa gtgcaaggct 1140

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 agccttgacct agcttggtaaa aggtcttctat cccagcgaca gtgggagagc 1320  
 aatggggcagc cggagaacaa ctacaagacc acgctctccc tgctggagtc cgacggctcc 1380  
 ttgcgctctc atagcaagct caccgtggag aagagcaggt ggcagcaggg gaactgtctc 1440  
 tcatgtcccg tgatgcata ggtctcgac aaccactaca gcgagaagag cctctccctg 1500  
 tccccgggta aatga  
 1515

<210> 381  
 <211> 1521  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polynucleotide

<400> 381  
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 gtcataattg aggtcacaat gacttcgagg gccagctcaa gtgtaagtta gctgtcatct 120  
 ccaggggaga aggtcacaat ctccccaa ccttgattt atgccccatc caactggctt 180  
 taccagcaga acgacagatc ctccccaa ccttgattt atgccccatc caactggctt 240  
 tctggagctc ctgctcgctt cagtggcagt ggttctggga cttcttactc tctcacattc 300  
 agcagagttg aggtcgaaga tgctgccact tttactgccc agcagtgagg ttttaacca 360  
 cccacgttcc gtgctgggac caagtggag ctgaaagatg gcggtggctc gggcggtgtg 420  
 ggatctggag gagggtggag ctctcaggt tatctacagc agtctggggc tgacgttggt 480  
 aggcctgggg cctcagtgaa gatgtcctgc aaggctcttg gctacacatt taccagtac 540  
 aatatgcact gggtaaaaga gacacctaga cagggtcctg aatggattgg agctatttat 600  
 ccaggaatgt gtgatcttc ctacaatcag aagtccaagg gcaaggccac actgactctga 660  
 gacaaatcct ccagcacagc ctacatcgag ctacagcagc tgacatctga agactctgag 720  
 gttctatttt gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 gacacatttc ccaggttcac cgtctcttct gatcaggagc cccagcagcc ccaaatcttc tgacaaaact 840  
 gttctatttt gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 cacacatttc ccaggttcac cgtctcttct gatcaggagc cccagcagcc ccaaatcttc tgacaaaact 840  
 ccccaaaact caccgtcccc agcacttgaa ctctcggggc gacgcgtcagt ctctctcttc 900  
 ccccaaaact caccgtcccc agcacttgaa ctctcggggc gacgcgtcagt ctctctcttc 900  
 gtggagctga ccagagaaca cctcatgac cctcatgac cctcatgac cctcatgac 960  
 gtgcataatt ccagagaaca cctcatgac cctcatgac cctcatgac cctcatgac 1020  
 agcttctcta cgtctctga ccagagctgg tcccgagccc aatggatttc atgcgttggt 1080  
 tccaacaaag ccttcccagc ccccatcgag aaaaactct ccaagccaa agggcagccc 1140  
 ccagacacac aggtgtacac cctgccccca cctgccccca ccaagccaa agggcagccc 1200  
 agcctgacct gccttggtcaa aggtctctat cccagcgaca agatgaccga gtgggagagc 1260  
 aatgggcagc cggagaacaa ctacaagacc acgctctccc tgctggagtc ttttaacctc 1320  
 ttctaccttc atagcaagct caccgtggag aagagcaggt ggcagcaggg gaactgtctc 1380  
 tcatgtccg tgatgcata ggtctcgac aaccactaca gcgagaagag cctctccctg 1440  
 tccccgggta aatgatctag a  
 1521

<210> 382  
 <211> 1515  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polynucleotide

<400> 382  
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 gtcataattg aggtcacaat gacttcgagg gccagctcaa gtgtaagtta catgcatctg 120  
 ccaggggaga aggtcacaat ctccccaa ccttgattt atgccccatc caactggctt 180  
 taccagcaga acgacagatc ctccccaa ccttgattt atgccccatc caactggctt 240  
 tctggagctc ctgctcgctt cagtggcagt ggttctggga cttcttactc tctcacattc 300  
 agcagagttg aggtcgaaga tgctgccact tttactgccc agcagtgagg ttttaacca 360  
 cccacgttcc gtgctgggac caagtggag ctgaaagatg gcggtggctc gggcggtgtg 420  
 ggatctggag gagggtggag gatctcggt tatctacagc agtctggggc tgactgattt 480  
 aggcctgggg cctcagtgaa gacacctaga cagggtcctg gctacacatt taccagttac 540  
 aatatgcact gggtaaaaga gacacctaga cagggtcctg aatggattgg agctatttat 600  
 ccaggaatgt gtgatcttc ctacaatcag aagtccaagg gcaaggccac actgactctga 660  
 gacaaatcct ccagcacagc ctacatcgag ctacagcagc tgacatctga agactctgag 720

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cacacatccc caccgtcccc agcactcgaa ctctctgggg gaccgtcagt ctctctcttc 900  
cccccaaac ccaaggacac cctcatgac tcccgagacc ctgaggtcac atgctggtg 960  
gtggacgtga gccacgaaga cctgaggtc aagttcaatt ggtacgtgga cggctggag 1020  
gtgcataatt ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080  
agcgtctcca cgtctctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140  
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cgagaaacac aggtgtacac ctgccccca ctgccccca agatgaccaa gaaccaggtc 1260  
agcctgacct gctgtgtcaa aggtctctat cccagcgaca tcgctgtgga gtgggaagag 1320  
aatggcgacg cggagacaaa ctacaagacc acgctctccg tctgtgactc cgacggtccc 1380  
ttcttctcgc ccagcaagct caccgtggag aagagcaggt ggacgaggg gaacgtcttc 1440  
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<211> 1515  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> fusion polynucleotide

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ccaggggaga aggttcacaa gacttgcagg gccagctcaa gttaagtta caagcactgg 180  
taccacgaga agccaggatc ctcccccaaa ccttgattt atgccccatc caactgggtc 240  
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acagagatgg aggtcgaga tgctgccact tattaactgc agcagtgag ttttaacca 360  
cccacgttgc gtgctgggac caagctggag ctgaaagat gcggtggtc ggcggtgtgt 420  
ggatctggag gaggctggag ctctcaggct tatctacagc agtctggggc tgagctgtgt 480  
agggctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact ggttaaaaga gacacctaga caggggctcg aatggaattg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatctt ccagcacagc ctacatgcag ctccagcagc tgacattcga agactctcgc 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgttactt cgaatgtctc 780  
ggcacaggga ccacggcac cgtcttctct gatcaggagc ccaaatcttc tgacaaaact 840  
cacacatccc caccgtcccc agcactgaa ctctctgggg gaccgtcagt ctctctcttc 900  
cccccaaac ccaaggacac cctcatgac tcccgagacc ctgaggtcac atgctgtgtg 960  
gtggacgtga gccacgaaga cctgaggtc aagttcaatt ggtacgtgga cggctggag 1020  
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agcgtctcta ccgtcttcca ccaggactgg ctgaatggca aggagtacaa gtgcaagttc 1140  
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agcctgacct gctgtgtcaa aggtctctat cccagcgaca tcgctgtgga gtgggaagag 1320  
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ttctactctg ccagcaagct caccgtggac aagagcaggt ggacgaggg gaacgtcttc 1440  
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tcccgggta aatga

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<211> 1515  
<212> DNA  
<213> Artificial Sequence  
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<223> fusion polynucleotide

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ccaggggaga aggttcacaa gacttgcagg gccagctcaa gttaagtta caagcactgg 180  
taccacgaga agccaggatc ctcccccaaa ccttgattt atgccccatc caactgggtc 240  
tctggagtcc ctgctgctt cagtggcagt gggctggtga cctcttactc tctcaactc 300

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 agcagagtgg aggctgaaga tgctgcacac tattactgcc agcagtggag ttttaaccaca 360  
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 ggaatctggag gaggctggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
 aggcctgggg cctcagtgaa gatgtctctg aaggcttctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaatctct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctcgc 720  
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 ggacacagggg cgcgtctcac cgtctcttct gatcaggagc ccaaatcttc cgaacaaact 840  
 cacacatccc caccgtcccc agcacctgaa ctctgggggg gaccgtcagt ctctctcttc 900  
 ccccaaaac ccaaggacac cctcatgatc tcccgagacc ctgaggtcac atgcgtgggtg 960  
 gtggacgtga gccacgaaga cctcagagtc aagtccaact ggtagctgga cggcggtggag 1020  
 gtgcataatg ccaagacaaa gcgcggggag gagcagtaca acagcacgta ccggtgggtc 1080  
 agcgtctctca ccgtctctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140  
 tccaacaagg tctctccagc cccatcgcag aaaaacact ccaagccaa agggcagccc 1200  
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 agcctgacct gcctggtcaa aggcctctat cccagcgaca tcgctggga gtggagagac 1320  
 aatggggcagc cggagaaaca ctacaagacc acgcctccg tgctggactc gcagcgtctc 1380  
 ttccctctcg ccagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440  
 tcatgcttcg tgaigcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500  
 tccccgggta aatga 1515

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 <211> 500  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 385  
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 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 80 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285

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 290 295  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 305 310 315  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 320 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Tyr Asn Ser Thr  
 340 345 350 355  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 360 365 370 375  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 380 385 390 395  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 400 405 410 415  
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 420 425 430 435  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 440 445 450 455  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 460 465 470 475  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Tyr Ser Lys Leu Thr  
 480 485 490 495  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 500 505  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 510 515  
 Ser Pro Gly Lys 500

<210> 386  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide

<400> 386  
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220

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 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn Thr Tyr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
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<210> 387  
 <211> 500  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> fusion polypeptide

<400> 387  
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 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270 275  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
 280 285 290 295  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 300 305 310 315  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 320 325 330 335  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 340 345 350 355  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 360 365 370 375  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 380 385 390 395  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 400 405 410 415  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 420 425 430 435  
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Met Thr Lys Asn Gln Val  
 440 445 450 455  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 460 465 470 475  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 480 485 490 495  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Ala Ser Lys Leu Thr  
 500 505 510 515  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 520 525 530 535  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 540 545 550 555  
 Ser Pro Gly Lys  
 560 565 570 575 580 585 590 595 600

<210> 388  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide

<400> 388  
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95



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 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Ala Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 389  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide

<400> 389  
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 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Leu Lys  
 115 120 125  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 385 390 395 400  
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Ala Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475 480  
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 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 390  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> 5' oligo to mutat IgG1

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<400> 390
gttggtgatac aggagcccaa atcttctgac aaaactcaca catg 44

<210> 391
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to mutate IgG1

<400> 391
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<210> 392
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to mutate IgG1

<400> 392
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cct 63

<210> 393
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcatctg 180
tctggagctc cgtctcgctt ctccccaaa ccttggattt atgccccatc caacctggct 240
agcagagtgg aggttgaaga tgctgccact tattactgcc agcagtgagg agtctggggc tgagctgggtg 300
ccacaggtct gtcgtgggac caagctggag ctctcaggct tatctacagc gcggtggctc gggcgtgggtg 360
ggatctggag aggtgggagg gatctcctgc aagggtctctg gctacacatt taccagttac 420
agccctgggg cctcagtgaa gacacctaga caaggctcagg aagttcaagg agtctgattgg agctatttat 480
aatatgacct gggtaaagca ctacaatcag atcagcagcc ccaaatcttc tgcataactga 540
ccaggaatag gtgatacttc ctacatgcag ctacagcagg agtgcagctg gcaaggccac actgacttgta 600
gacaaatcct ccagcacagc gtgtgtactat agtaactctt gatcaggagc cctctctctc 660
gtctatttct gtgcaagagt cgtctctctc gatcaggagc cctctctctc 720
ggcacaggga ccacggtcac cgtctctctc gatcaggagc cctctctctc 780
cacacatgac caccgtgccc agcacctgaa ctctctgggg gaccgtcagt ctctctctc 840
ccccaaaaa ccaaggacac cctcatgac tcccggagcc ctgaggtcac atgcgtgggtg 900
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tccaaacacg cctctctcag ccccatcgag aaaaacaatt tcccgggatg agctgaccaa gaaccaggctc 1200
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aattgggacct tcttctctct acagcaagct caccgtggag accactata cctctctctg 1380
tcatgtctcg tgatgatga ggtctctgac aaccactata cgcagaagag cctctctctg 1440

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
tctccgggta aatgatctag a 1521

<210> 394  
<211> 1521  
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<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

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gtcataattg ccagaggaca aattgttctc tccagctctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgctctgg 180  
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
tctggagttc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcaaatc 300  
agcagagtgg aggtctgaaga tgctgccact tattactgcc agcagtgagg ttttaacca 360  
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ggatctggag gaggtgggag gatgtctctg aagggctctg gctacacatt taccagttac 480  
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aatgtccact gggtaaagca ctacaatcag atgttcaagg gctacacatt taccagttac 600  
ccaggaaagt gtgatacttc ctacaatcag atgttcaagg gctacacatt taccagttac 660  
gacaaatcct ccagcacagc ctacatcgag atgttcaagg gctacacatt taccagttac 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt gacgtctgg 780  
ggcacaaggc ccaggtcac cgtctcttct gatcaggagc ccaaatcttg tgacaaact 840  
cacacatctc caccgtgcc agcacctgaa ctctctgggg gaccgtcagt ctctctctc 900  
cccccaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgcgtgtg 960  
gtggacgtga gccacgaaga cctgaggtc aagtccaact ggtactgtga cggcgtggag 1020  
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080  
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cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgcgcaa gaacacagtc 1260  
agctgtacct gctcgttcaa aggtcttctat cccagcgaca tcgctgtgga gtggagagtc 1320  
aatgggcagc cgggaagcaa ctacaagacc acgcctcccg tgcgtgactc cgacagcttc 1380  
ttcttctctc acagcaagc caccgtggag aagagcaggt ggcagcaggg gaacgtcttc 1440  
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tctccgggta aatgatctag a 1521

<210> 395  
<211> 1521  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

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ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgctctgg 180  
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
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agcagagtgg aggtctgaaga tgctgccact tattactgcc agcagtgagg ttttaacca 360  
cccacgttcg gtgctgggac caagctggag ctctcaggct tatctacagc agtctgggct gggcggtgg 420  
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aggtctgggg cctcagtgaa gatgtctctg aagggctctg gctacacatt taccagttac 540  
aatatgcact gggtaaagca gacacctaga aagttcaagg gcaaggccac actgacttga 600  
ccaggaaagt gtgatacttc ctacaatcag atgttcaagg gcaaggccac actgacttga 660  
gacaaatcct ccagcacagc ctacatcgag atgttcaagg gcaaggccac actgacttga 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
ggcacaaggc ccaggtcac cgtctcttct gatcaggagc ccaaatcttg tgacaaact 840  
cacacatctc caccgtcccc agcacctgaa ctcttggggc gaccgtcagt ctctctctc 900  
cccccaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgcgtgtgg 960  
gtggcagtgga gccacgaaga cctgaggtc aagtccaact ggtactgtga cggcgtggag 1020  
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 cgagaaccac aggtgtacac cctgcgccca tcccgggatg agctgaccac gaaccaggtcc 1260  
 accctgacct gcctgtgtcaa aggtctctat cccagcgaca tcgctgtgga gtgggagagc 1320  
 aatgggcagc cggagaacaa ctacaagacc acgctcccg tgctggactc cgacggctcc 1380  
 ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440  
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<210> 396  
 <211> 500  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> fusion polypeptide

<400> 396  
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 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 260 265 270  
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 305 310 315 320  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 325 330 335  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Tyr Asn Ser Thr  
 340 345 350  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 355 360 365  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 370 375 380  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 385 390 395  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 405 410 415  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 420 425 430  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 435 440 445  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 450 455 460  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 465 470 475  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 485 490 495  
 Ser Pro Gly Lys  
 500

<210> 397  
 <211> 500  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> fusion polypeptide

<400> 397  
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 80 85 90  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 160 165 170  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 175 180 185  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 190 195 200  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 205 210 215  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 220 225 230  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 235 240 245  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 250 255 260  
 Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu  
 265 270 275  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 280 285 290  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 295 300 305  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 310 315 320

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 Ser Pro Gly Lys  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395  
 400 405 410 415  
 420 425 430 435  
 440 445 450 455  
 460 465 470 475 480 485 490 495  
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<210> 398  
 <211> 500  
 <212> PRT  
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 <220>  
 <223> fusion polypeptide

<400> 398  
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 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 Asp Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser  
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 260 265 270  
 Cys Asp Lys Thr His Thr Cys Pro Ser Pro Ala Pro Glu Leu Leu  
 275 280 285  
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 290 295 300  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser  
 305 310 315  
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Ser  
 320 325 330  
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
 335 340 345  
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 350 355 360  
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 365 370 375  
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
 380 385 390  
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
 395 400  
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 405 410 415  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 420 425 430  
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
 435 440 445  
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
 450 455 460  
 Met His Glu Ala Leu His Asn His Thr Gln Lys Ser Leu Ser Leu  
 465 470 475  
 Ser Pro Gly Lys  
 480 485 490 495 500

<210> 399  
 <211> 793  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

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 gacatagtgc tgactcagac tccagccact ctgtctctaa ttcctggaga aagagtccaca 120  
 atgacctgtga agaccagtcga gaattattggc acaatcttac actggtatca ccaaaaacca 180  
 aaggaggctcc caagggtctt catcaagtat gcttcgcagt ccattctcgg gatcccctcc 240  
 agattcagtg gcagtggttc gaaacacagat ttactctcta gcatcaataa cctggagcct 300  
 gatgatatcg gaattatata ctgtcaacaa agtagaagct ggcctgtcac gttcggctct 360  
 ggacacaaag tggagataaa acggggtggc ggtggctcgg gcggaggtag gtcgggtggc 420  
 ggcgagatctc aggtcaagct ttacagctac taggggaacc tggggcctca 480  
 ctgaaactgt cctgcaagac cctgcagtag agtagaagct atactatata ttcttgggtg 540  
 aaacagaagc ctggagaag ctaggcaag ccagggcaag ctataggtag aatatgggtg 600  
 acaagctaca atcaaaaatt cagcctgaca tctgagtagg ttatgggtgg aatctctagc 660  
 acagcctaca tggaaactcag cagcctgaca tctgagtagg ttatgggtgg aatctctagc 720  
 agaagggcgg tagcgacggg ccactgtatg gactactggg gtcaggggat ccaagtacc 780  
 gtctctcctg atc 793

<210> 400  
 <211> 264  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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 Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn  
 35 40 45  
 Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro  
 50 55 60  
 Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser  
 65 70 75 80  
 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn  
 85 90 95  
 Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg  
 100 105 110  
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg  
 115 120 125  
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln  
 130 135 140  
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser  
 145 150 155 160  
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr  
 165 170 175  
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly  
 180 185 190  
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln  
 195 200 205  
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met  
 210 215 220  
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala  
 225 230 235 240  
 Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly  
 245 250 255  
 Ile Gln Val Thr Val Ser Ser Asp  
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<210> 401  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> oligonucleotide primer

<400> 401  
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36

<210> 402  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide primer

<400> 402  
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44

<210> 403  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> oligonucleotide primer

<400> 403  
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<210> 404  
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<400> 404  
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<210> 405  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 405  
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<210> 406  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 406  
gtgttatcg atctcgagtt atcaggacgc ttcggaggta gatgcgtc 48

<210> 407  
<211> 657  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 407  
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cgctgacaga ggcgcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 180  
gggcacacgc agctcctcgc cgagctgctc gcctcctcgc ggcgccacga cctgctcggg 240  
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tgtgcagcat ttaacgtcat atgtgataat gtggggaag attggagaag gctggtcgtg 360  
cagctcaag tctcagacac caagatcgac agcatcgagg acagataccc ccgcaacctg 420  
acagagctg tgcgggagtc actgagaatc tgggaagaaca cagagaagga gaacgcaaca 480  
gtggccaccc tgggtggggc tctcaggtcc tgcagatga acctggtggc tgacctgtgta 540  
caagaggttc agcagggccg tgacctccag aacaggagtg gggccatgtc cccgatgtca 600  
tggaactcag acgcatctac ctccgaagcg tcttgataac tcgagatcga taacaac 657

<210> 408

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 408

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Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
 35
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
 50
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
 65
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly
 80
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
 95
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
110
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
125
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
140
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
155
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
170
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
185
Glu Ala Ser 195 200 205
210

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<210> 409

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 409

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<210> 410

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 410

gtgttttcga acccagaaaa taataaaggc cactgttact agcaagctat agcaagccag 60

<210> 411

<211> 32

<212> DNA

<213> Artificial Sequence

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<211> 33
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<220>
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<400> 412
gttgtttcga acccgaaaa taataaaggc cac                                33
<210> 413
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 413
gttgaggatc ctctgctcc catcctgg                                28
<210> 414
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<220>
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<400> 414
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<212> DNA
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<220>
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<400> 415
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<210> 416
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 416
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<210> 417
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 417

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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 ctggagcgcg tgcagagtgg cctggacctg ttacgggtgc tgcctggaagca gaacgacctg 180  
 gagcgcgggc acaccgggctt gctgcgcgag ttgtctgacct cgtcgcgcgc acacgatcta 240  
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 gcccgcgagc tgaaggtgtc tgaggccaag atggatggga ttgaggagaa gtacccccga 420  
 agtctgagtg agcgggttaag ggagagctct aaagtctgga agaattgctga gaagaagaac 480  
 gcctcggttg ccgactgtgt caagcgcgtg cggacctgca ggctgaattc ggtggctcag 540  
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 gattcaactg tgtcttcttc agaaaacccc tgactcgaga tcgat 645

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 <211> 210  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> fusion polypeptide

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 Arg Glu Arg Val Ser Lys Arg Lys Leu Glu Arg Val Glu Ser Gly Leu  
 35 40 45  
 Asp Leu Phe Thr Val Leu Leu Glu Glu Asn Asp Leu Glu Arg Gly His  
 50 55 60  
 Thr Gly Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu  
 65 70 75 80  
 Leu Glu Arg Leu Asp Asp Phe Glu Ala Gly Thr Ala Thr Ala Ala Pro  
 85 90 95  
 Pro Gly Glu Ala Asp Leu Glu Val Ala Phe Asp Ile Val Cys Asp Asn  
 100 105 110  
 Val Gly Arg Asp Trp Lys Arg Leu Ala Arg Glu Leu Lys Val Ser Glu  
 115 120  
 Ala Lys Met Asp Gly Ile Glu Glu Lys Tyr Pro Arg Ser Leu Ser Glu  
 130 135 140  
 Arg Val Arg Glu Ser Leu Lys Val Trp Lys Asn Ala Glu Lys Lys Asn  
 145 150 155 160  
 Ala Ser Val Ala Gly Leu Val Lys Ala Leu Arg Thr Cys Arg Leu Asn  
 165 170 175  
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 Glu Asn Met Ser Pro Val Leu Arg Asp Ser Thr Val Ser Ser Ser Glu  
 195 200 205  
 Thr Pro  
 210

<210> 419  
 <211> 48  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> oligonucleotide

<400> 419  
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48

<210> 420  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<220>
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<400> 420
gttgttatcg atctcgagct agtgataaaa gtacagttct ttgc          44
<210> 421
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 421
gttgtttcga acatggattt ccagagttgt cttatgcta ttgctg          46
<210> 422
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 422
gttgttatcg atctcgagtc attagggagg gaagaagagc ttcttcgc          48
<210> 423
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 423
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<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

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<211> 45
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<213> Artificial Sequence

<220>
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<211> 48

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 426

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48

18

EXPRESS MAIL NO:

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